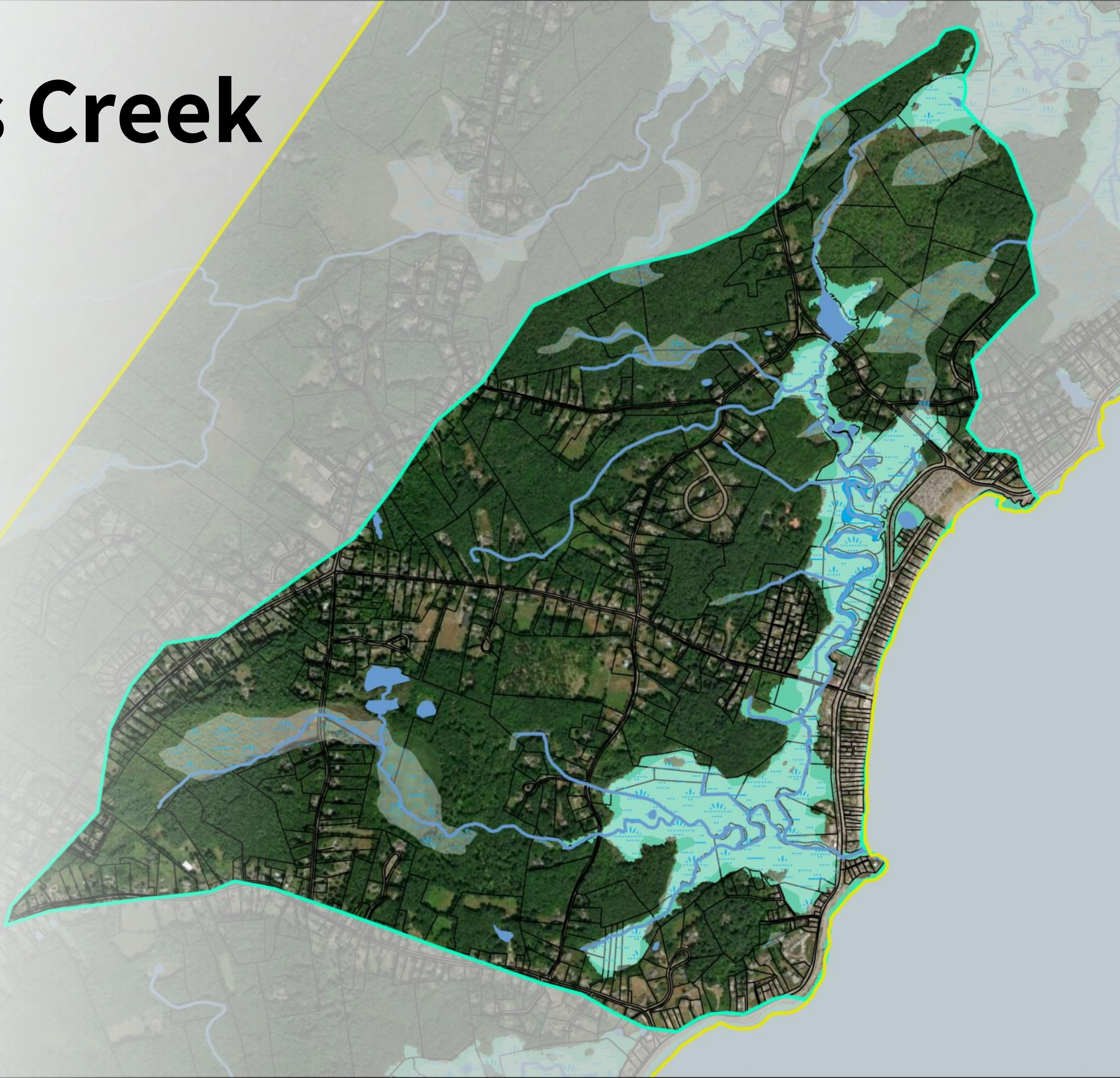
Restoring Parsons Creek
Rye CWSRF

Rye Select Board Meeting
June 12, 2023



Luke Frankel & Laura Diemer
FB Environmental Associates

Outline

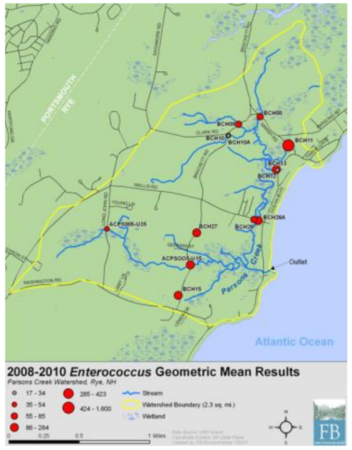
- Watershed Background
- Water Quality Monitoring Efforts
- Historical Monitoring Results
- 2022 Monitoring Results
- 2022 PhyloChip Results
- PhyloChip Discussion
- Next CWSRF Project

Parsons Creek Watershed

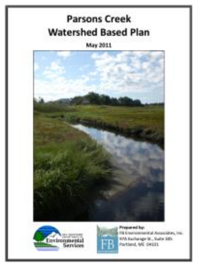
- Comprised of Class B waterbodies
- 5 different assessment units
    - 3 freshwater rivers (Parsons Creek East and 2 unnamed)
    - 1 lake (Marsh Road Pond)
    - 1 estuary (Parsons Creek)
- Enterococci criteria:
    - 104 MPN/100mL (single sample)
    - 35 MPN/100mL (geomean)
- Bacteria Impairments:
    - Parsons Creek
    - Parsons Creek East

Water Quality Monitoring Efforts

- Preliminary bacteria source identification (2008)
- Parsons Creek Watershed Based Plan (2011)
- Regular Enterococci monitoring (2013-Present)
- Additional monitoring efforts:
  - Canine scent detection (2013, 2015)
  - Beach seep monitoring (2015-2016)
  - Storm event monitoring (2017)
  - Groundwater monitoring (2018)
  - Nutrients (2017-2022)
  - PhyloChip (2022)




anine scent detection in 2013. ©FBE.


Parsons Creek Watershed Based Plan
May 2011

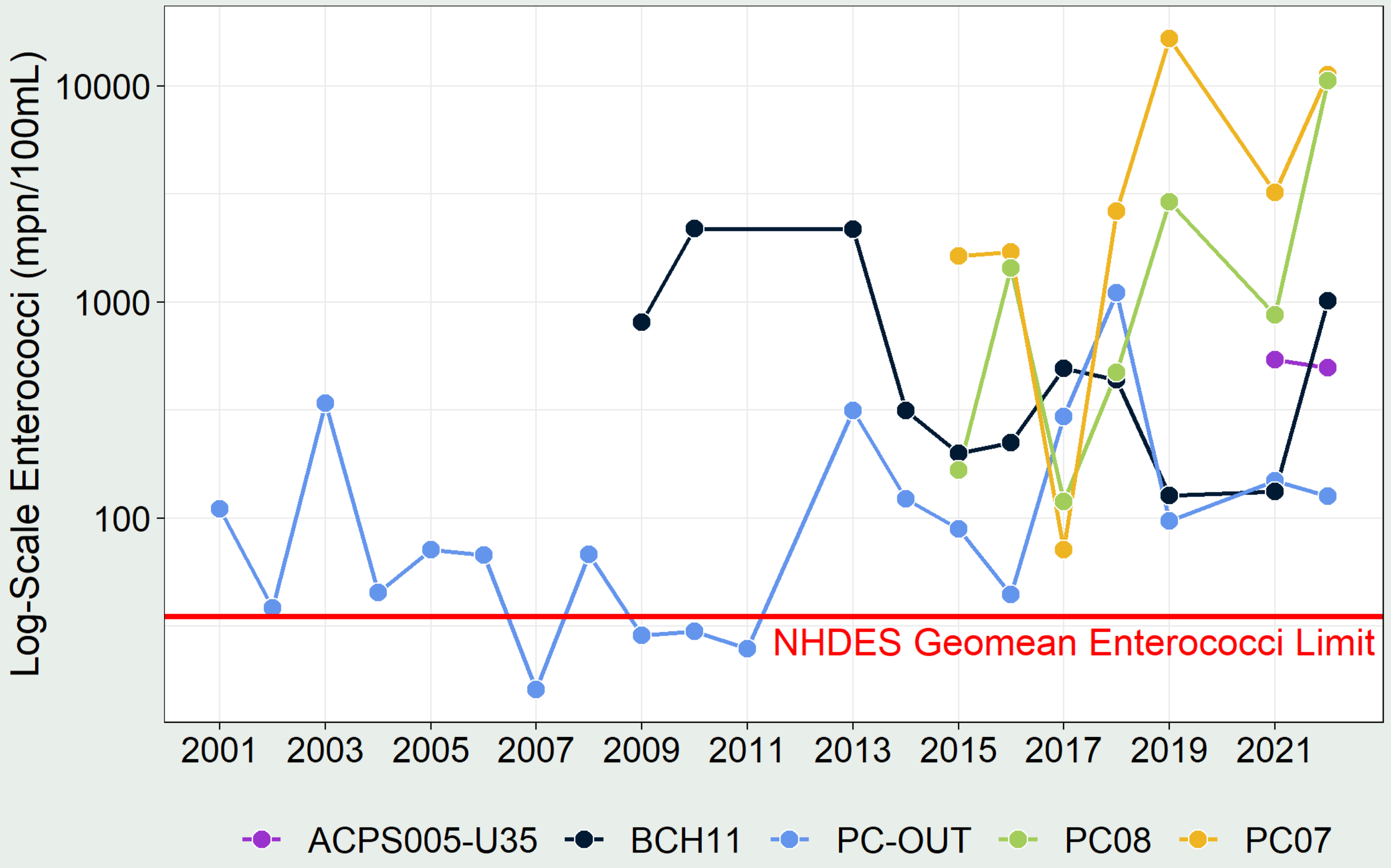

Sampling on June 1, 2023. ©FBE.

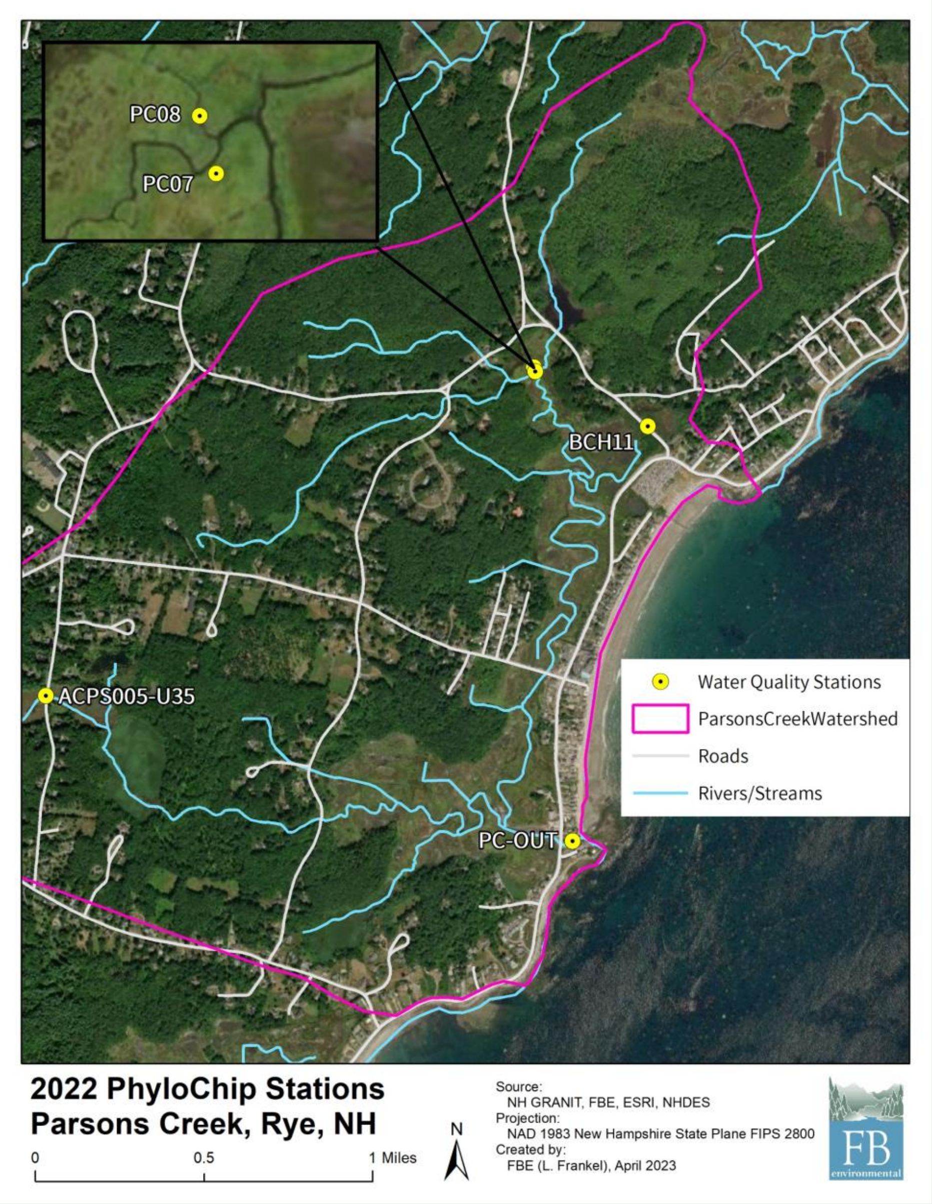

Beach seep monitoring in 2016. ©FBE.


Groundwater monitoring 2018. ©FBE.

Historical Monitoring Results

Enterococci continue to remain high in Parsons Creek



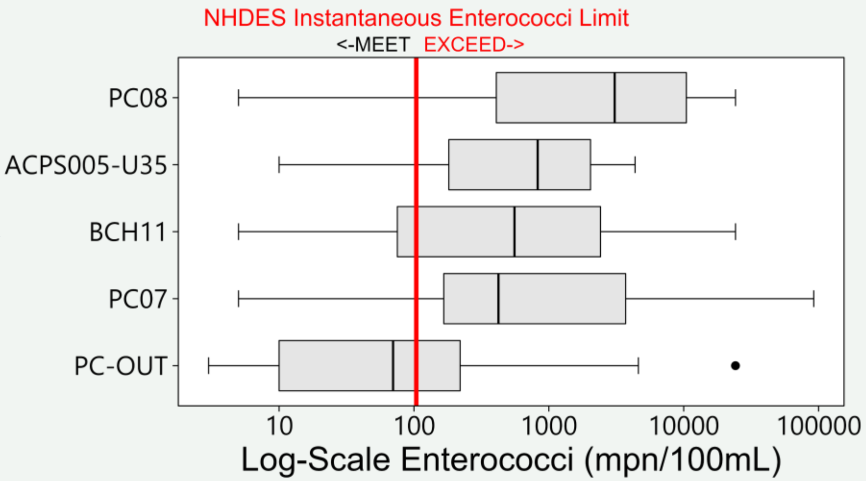


2022 PhyloChip Stations
Parsons Creek, Rye, NH

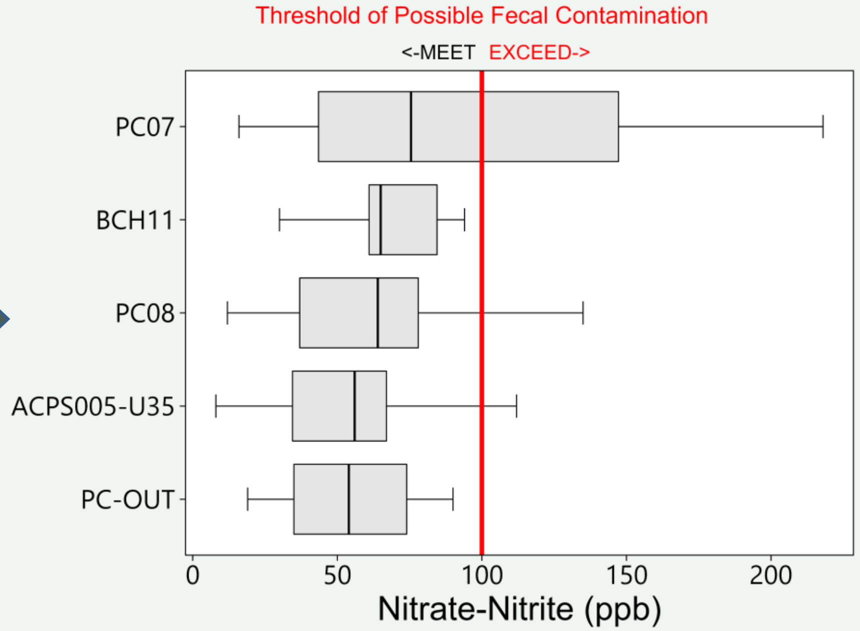
Source:
NH GRANIT, FBE, ESRI, NHDES
Projection:
NAD 1983 New Hampshire State Plane FIPS 2800
Created by:
FBE (L. Frankel), April 2023

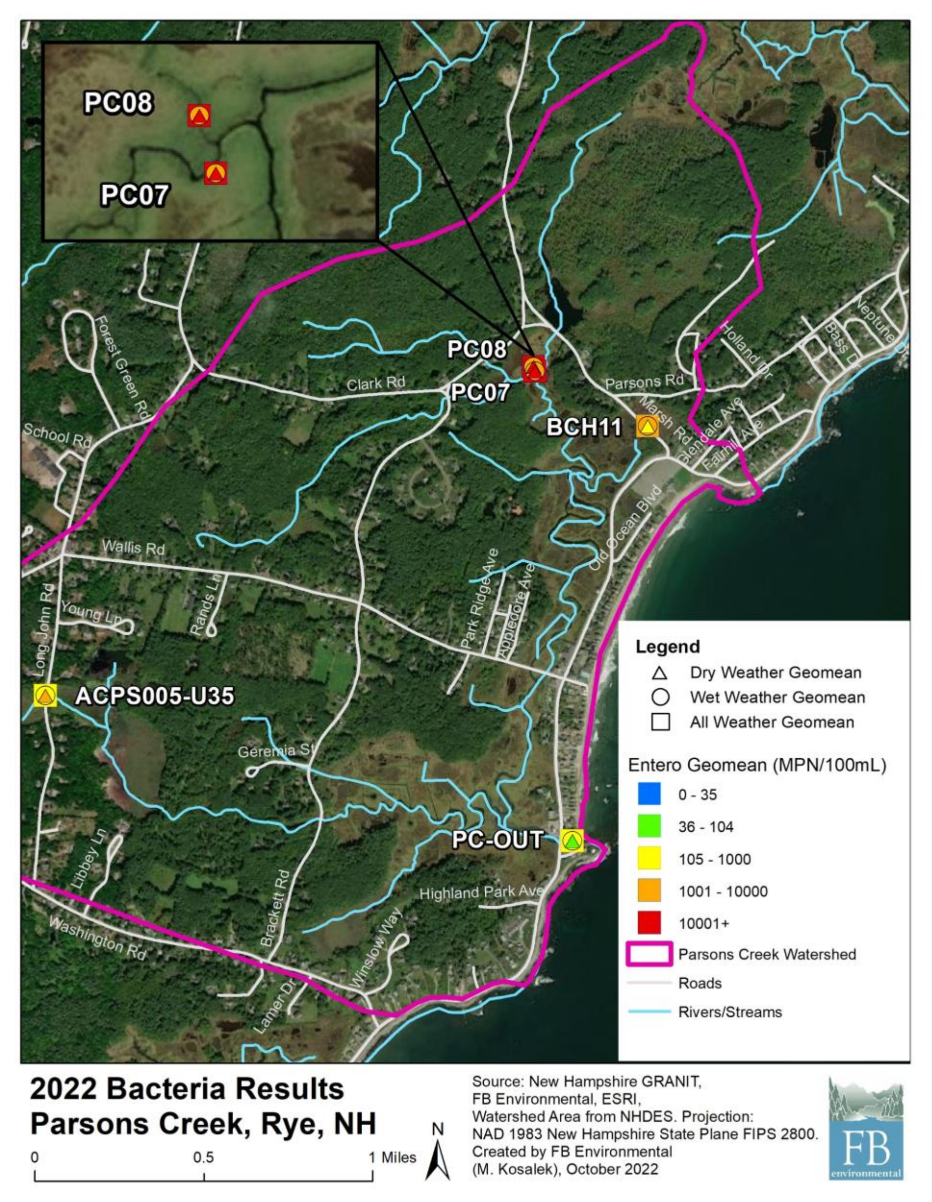
2022 Monitoring Results

Enterococci



Nutrients





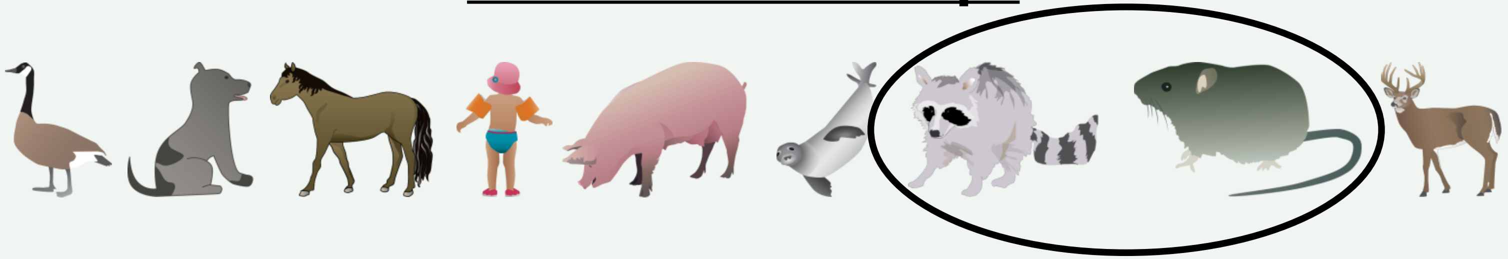
Source: New Hampshire GRANIT,
FB Environmental, ESRI,
Watershed Area from NHDES. Projection:
NAD 1983 New Hampshire State Plane FIPS 2800.
Created by FB Environmental
(M. Kosalek), October 2022

2022 PhyloChip Results

Sampling

- 5 events (2 wet, 3 dry)
- All 5 stations

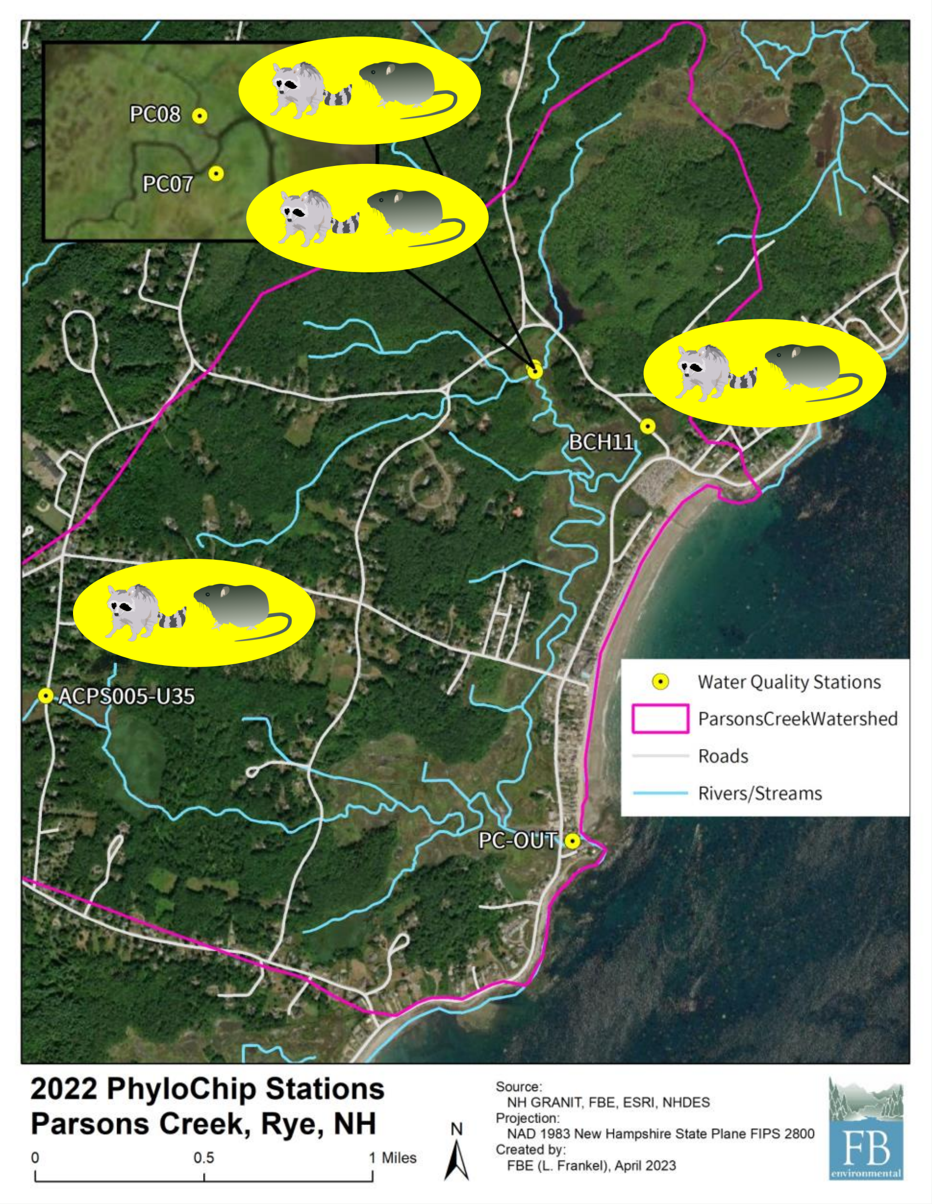
Nine Animal Groups



Predicted Contributions

🟡 Potential Source: 0.1 – 0.2

🔴 Clear Source: > 0.2



2022 PhyloChip Results

Potentially Harmful Bacteria

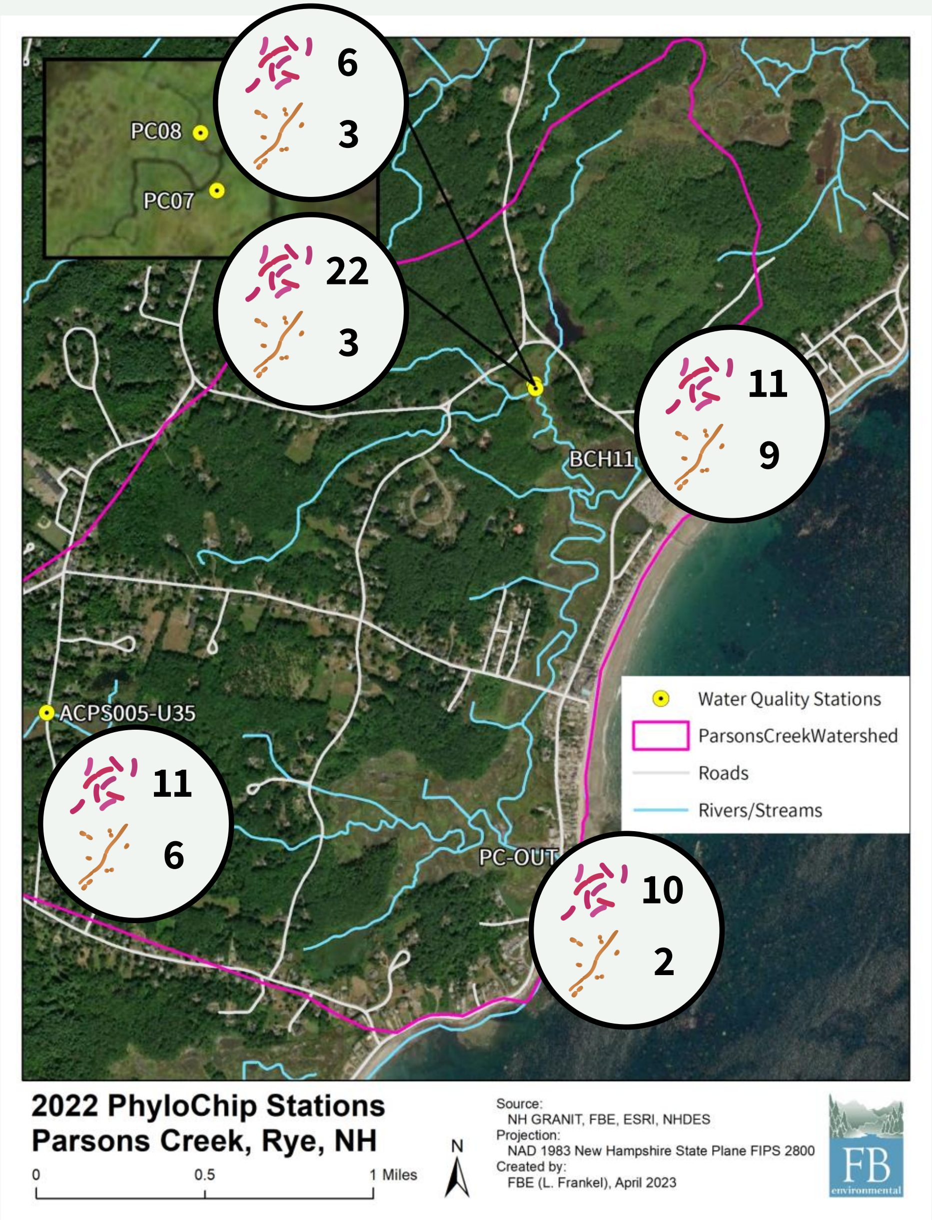
- Streptococcus

Strep throat; pink eye; meningitis; impetigo; bacterial pneumonia

- Staphylococcus

Skin infection

Max Number of Genera Present



2022 PhyloChip Stations
Parsons Creek, Rye, NH

Source:
NH GRANIT, FBE, ESRI, NHDES
Projection:
NAD 1983 New Hampshire State Plane FIPS 2800
Created by:
FBE (L. Frankel), April 2023

PhyloChip Discussion – No Human or Bird?

- Lack of sensitivity: The salt marsh likely altered and/or dampened the human fecal matter signature such that PhyloChip was unable to detect it.

Unlikely scenarios

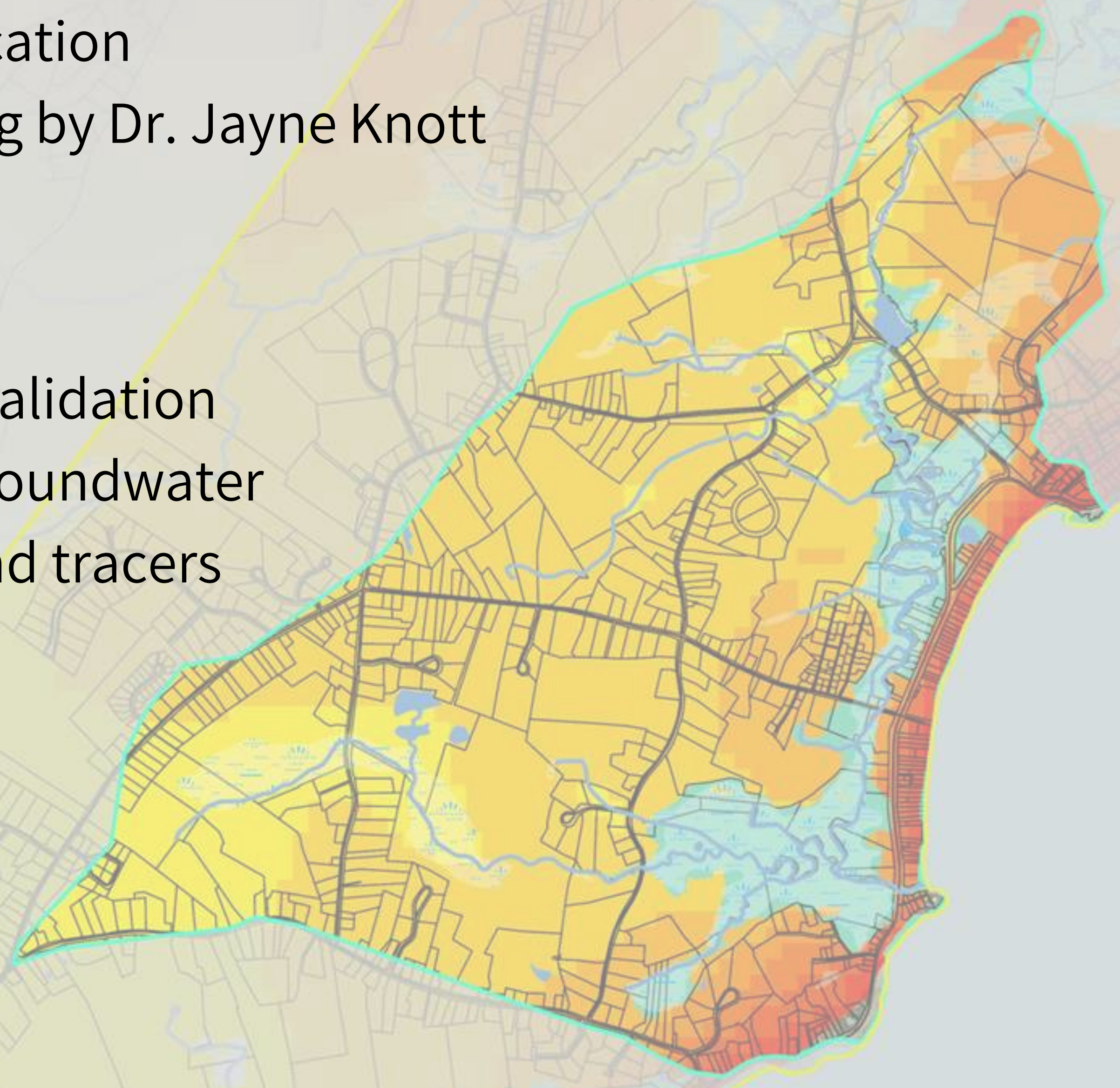
- Microbial mismatch: Microbial communities in Parsons Creek may not have matched those in Veracet's library, causing lower predicted contributions. The human and bird groups in the library use the largest set of samples, therefore this is unlikely.
- Matrix interference: Particulates in samples may have caused DNA extraction and processing issues. Thousands of bacteria commonly found in water were identified, making this unlikely.
- Low bacteria levels: Watershed management efforts have caused human waste contamination to be undetectable. Other efforts (canine scent detection, DNA ribotyping, Enterococci sampling) suggest that this is unlikely.

Next CWSRF

- Groundwater modeling and septic risk identification
  - 50ft x 50ft resolution groundwater modeling by Dr. Jayne Knott
  - Septic system elevations from site plans
  - Solute transport modeling of bacteria

- Water quality sampling for model calibration/validation
  - Expanding annual monitoring to include groundwater monitoring for water quality parameters and tracers

- Public outreach
  - Workshop for residents to learn about septic system maintenance and the results of the study

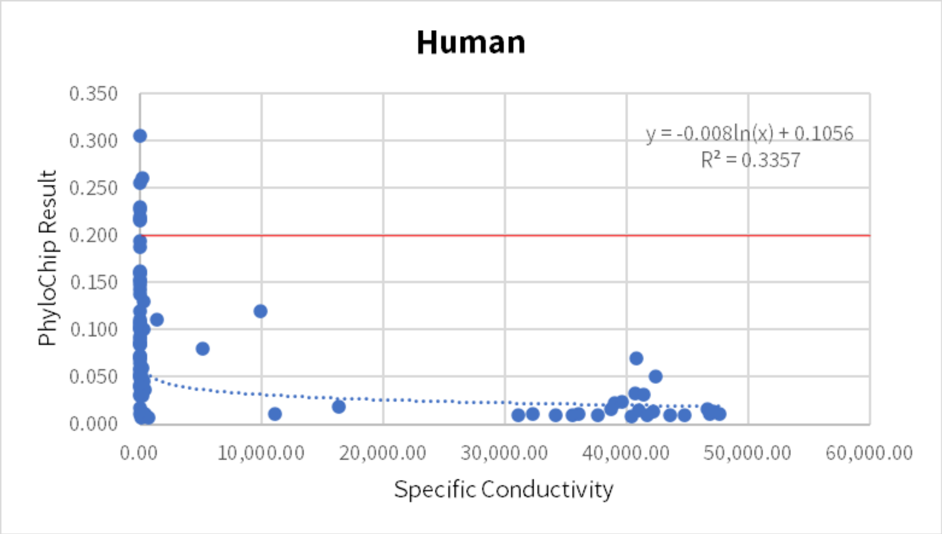


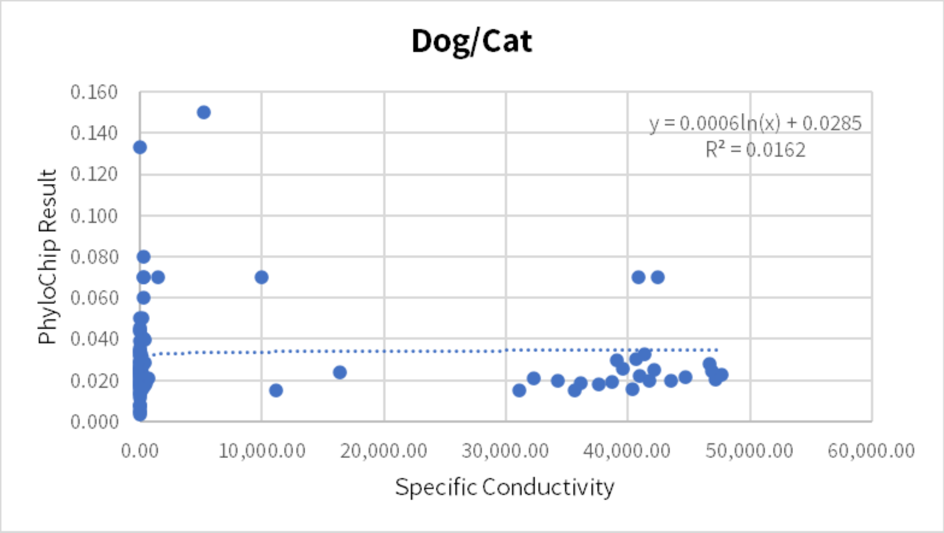
Questions?

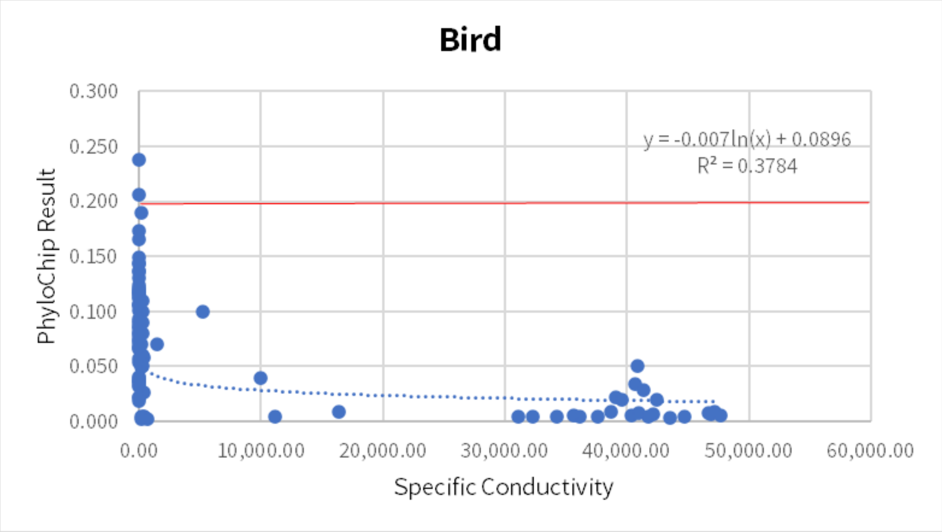
PhyloChip Predicted Contribution vs. Specific Conductivity

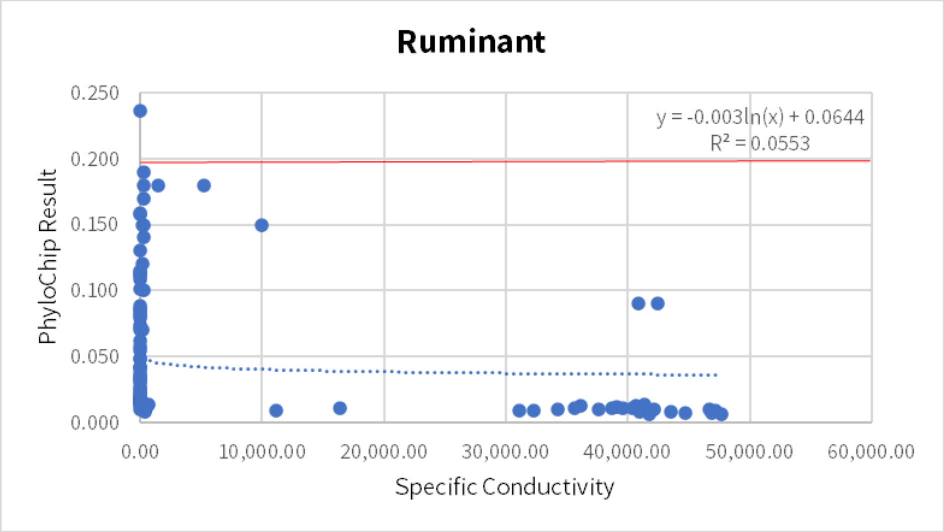
- 96 Samples

- 4 Studies
- Parsons Creek
  - Rye, NH
- Bride Brook
  - East Lyme, CT
- Ogunquit River
  - Ogunquit, ME
- Palmer River
  - Rehoboth, MA


Human


Dog/Cat


Bird


Ruminant

Bowen et al., 2009

- No significant difference in microbial community between fertilized and unfertilized marsh
- Salt marsh habitat zone has a stronger influence on the microbial community

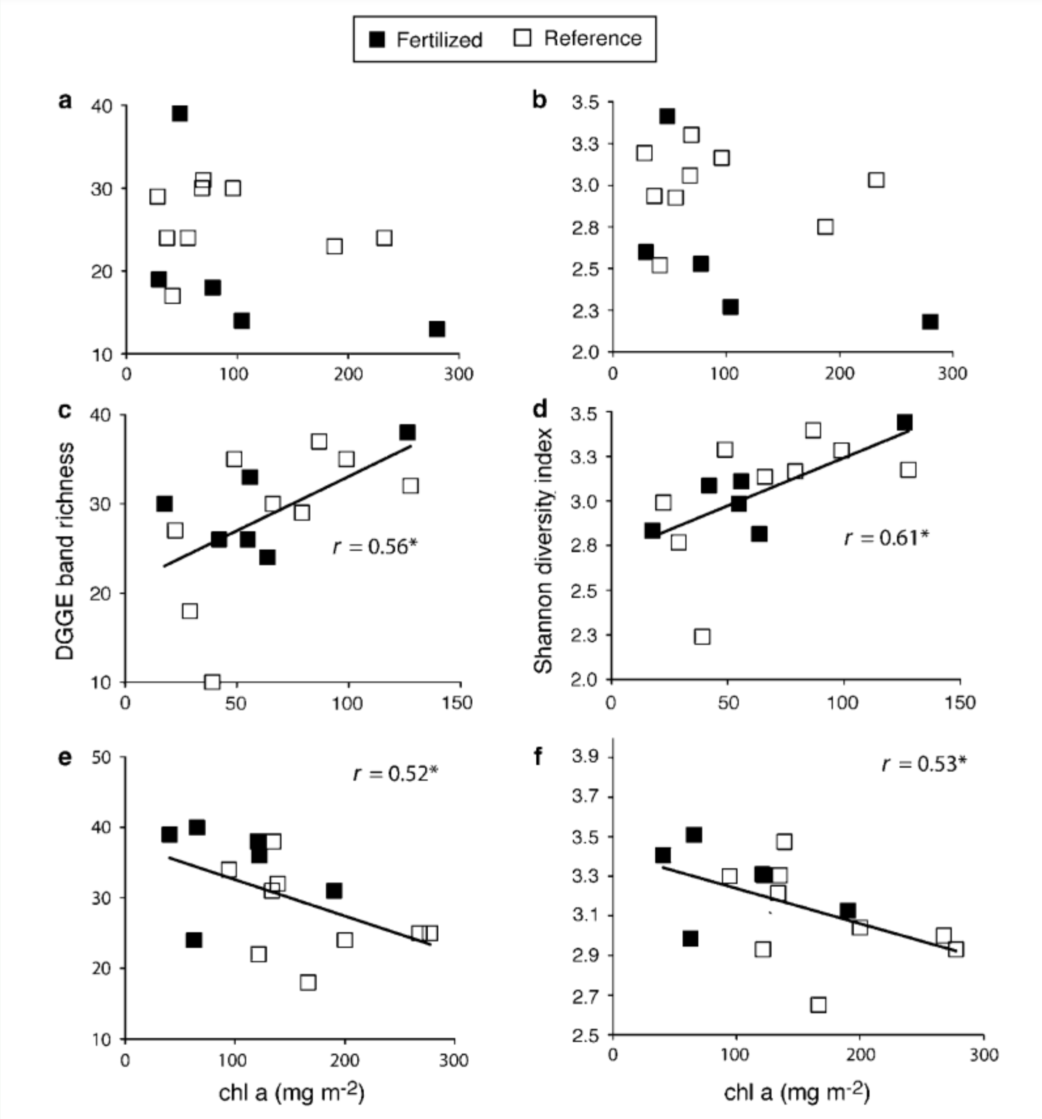
DGGE Band

Shannon Diversity

Filamentous Algae Zone

Mudflat Zone

Tall *S. alterniflora* Zone



Bowen, J., Crump, B., and Deegan, L. (2009). Salt marsh sediment bacteria: their distribution and response to external nutrient inputs. ISME J 3, 924–934. https://doi.org/10.1038/ismej.2009.44